

SEQUENCE LISTING

<110> SHINTANI et al.

<120> MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING BRAIN/NERVE CELL PROTECTIVE AGENT

<130> 20039.0001USWO

<140> 10/547,532

<141> 2005-08-31

<150> PCT/JP2004/002774

<151> 2004-03-04

<150> JP 2003-056885

<151> 2003-03-04

<150> JP 2003-106247

<151> 2003-04-10

<160> 21

<170> PatentIn version 3.1

<210> 1

<211> 288

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(288)

<223>

<220>

<221> sig_peptide

<222> (1)..(78)

<223>

<220>

<221> mat_peptide

<222> (79)..()

<223>

<400> 1

atg tgc tgt acc aag agt ttg ctc ctg gct gct ttg atg tca gtg ctg	48
Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu	
-25 -20 -15	
cta ctc cac ctc tgc ggc gaa tca gaa gca gca agc aac ttt gac tgc	96
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys	
-10 -5 -1 1 5	
tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc	144
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly	
10 15 20	
ttc aca cgg cag ctg gcc aat gaa ggc tgt gac atc aat gct atc atc	192
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile	

25	30	35	
ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa cag act	240		
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr			
40	45	50	
tgg gtg aaa tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg	288		
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met			
55	60	65	70

<210> 2
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 2	
Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu	
-25	-20
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys	
-10	-5
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly	
10	15
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile	
25	30
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr	
40	45
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met	
55	60
	65
	70

<210> 3
 <211> 288
 <212> DNA
 <213> Rattus norvegicus

<220>
 <221> CDS
 <222> (1)..(288)
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(75)
 <223>

<220>
 <221> mat_peptide
 <222> (76)..()
 <223>

<400> 3	
atg gcc tgc aag cat ctg ccc ttc ctg gct ttg gcg ggg gta ctg ctg	48
Met Ala Cys Lys His Leu Pro Phe Leu Ala Leu Ala Gly Val Leu Leu	
-25	-20
gct tac ctc tgc agc cag tca gaa gca gca agc aac ttt gac tgc tgc	96
Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys	
-5	-1
ctc acg tac aca aag aac gtg tat cat cat gcg aga aat ttt gtg ggt	144
Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly	
10	15
	20

ttc	aca	aca	cag	atg	gcc	gac	gaa	gct	tgt	gac	att	aat	gct	atc	atc	192
Phe	Thr	Thr	Gln	Met	Ala	Asp	Glu	Ala	Cys	Asp	Ile	Asn	Ala	Ile	Ile	
	25					30					35					
ttt	cac	ctg	aag	tcg	aaa	aga	tcc	gtg	tgc	gct	gac	cca	aag	cag	atc	240
Phe	His	Leu	Lys	Ser	Lys	Arg	Ser	Val	Cys	Ala	Asp	Pro	Lys	Gln	Ile	
40					45				50					55		
tgg	gtg	aaa	agg	att	ttg	cac	ctc	ctc	agc	cta	aga	acc	aag	aag	atg	288
Trp	Val	Lys	Arg	Ile	Leu	His	Leu	Leu	Ser	Leu	Arg	Thr	Lys	Lys	Met	
				60					65					70		

<210> 4
 <211> 96
 <212> PRT
 <213> Rattus norvegicus

<400>	4															
Met	Ala	Cys	Lys	His	Leu	Pro	Phe	Leu	Ala	Leu	Ala	Gly	Val	Leu	Leu	
-25					-20					-15					-10	
Ala	Tyr	Leu	Cys	Ser	Gln	Ser	Glu	Ala	Ala	Ser	Asn	Phe	Asp	Cys	Cys	
				-5				-1	1			5				
Leu	Thr	Tyr	Thr	Lys	Asn	Val	Tyr	His	His	Ala	Arg	Asn	Phe	Val	Gly	
	10						15				20					
Phe	Thr	Thr	Gln	Met	Ala	Asp	Glu	Ala	Cys	Asp	Ile	Asn	Ala	Ile	Ile	
	25					30				35						
Phe	His	Leu	Lys	Ser	Lys	Arg	Ser	Val	Cys	Ala	Asp	Pro	Lys	Gln	Ile	
40					45				50					55		
Trp	Val	Lys	Arg	Ile	Leu	His	Leu	Leu	Ser	Leu	Arg	Thr	Lys	Lys	Met	
				60					65					70		

<210> 5
 <211> 291
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(291)
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(81)
 <223>

<220>
 <221> mat_peptide
 <222> (82)..()
 <223>

<400>	5															
atg	gcc	tgc	ggt	ggc	aag	cgt	ctg	ctc	ttc	ctt	gct	ttg	gca	tgg	gta	48
Met	Ala	Cys	Gly	Gly	Lys	Arg	Leu	Leu	Phe	Leu	Ala	Leu	Ala	Trp	Val	
	-25						-20				-15					
ctg	ctg	gct	cac	ctc	tgc	agc	cag	gca	gaa	gca	gca	agc	aac	tac	gac	96
Leu	Leu	Ala	His	Leu	Cys	Ser	Gln	Ala	Glu	Ala	Ala	Ser	Asn	Tyr	Asp	
	-10					-5			-1	1				5		
tgt	tgc	ctc	tcg	tac	ata	cag	acg	cct	ctt	cct	tcc	aga	gct	att	gtg	144

Cys	Cys	Leu	Ser	Tyr	Ile	Gln	Thr	Pro	Leu	Pro	Ser	Arg	Ala	Ile	Val		
				10				15						20			
ggt	ttc	aca	aga	cag	atg	gcc	gat	gaa	gct	tgt	gac	att	aat	gct	atc	192	
Gly	Phe	Thr	Arg	Gln	Met	Ala	Asp	Glu	Ala	Cys	Asp	Ile	Asn	Ala	Ile		
			25					30					35				
atc	ttt	cac	acg	aag	aaa	aga	aaa	tct	gtg	tgc	gct	gat	cca	aag	cag	240	
Ile	Phe	His	Thr	Lys	Lys	Arg	Lys	Ser	Val	Cys	Ala	Asp	Pro	Lys	Gln		
		40					45				50						
aac	tgg	gtg	aaa	agg	gct	gtg	aac	ctc	ctc	agc	cta	aga	gtc	aag	aag	288	
Asn	Trp	Val	Lys	Arg	Ala	Val	Asn	Leu	Leu	Ser	Leu	Arg	Val	Lys	Lys		
	55					60				65							
atg																291	
Met																70	

<210> 6
 <211> 97
 <212> PRT
 <213> Mus musculus

Met	Ala	Cys	Gly	Gly	Lys	Arg	Leu	Leu	Phe	Leu	Ala	Leu	Ala	Trp	Val		
		-25					-20					-15					
Leu	Leu	Ala	His	Leu	Cys	Ser	Gln	Ala	Glu	Ala	Ala	Ser	Asn	Tyr	Asp		
	-10					-5			-1	1				5			
Cys	Cys	Leu	Ser	Tyr	Ile	Gln	Thr	Pro	Leu	Pro	Ser	Arg	Ala	Ile	Val		
			10					15					20				
Gly	Phe	Thr	Arg	Gln	Met	Ala	Asp	Glu	Ala	Cys	Asp	Ile	Asn	Ala	Ile		
		25					30					35					
Ile	Phe	His	Thr	Lys	Lys	Arg	Lys	Ser	Val	Cys	Ala	Asp	Pro	Lys	Gln		
	40					45					50						
Asn	Trp	Val	Lys	Arg	Ala	Val	Asn	Leu	Leu	Ser	Leu	Arg	Val	Lys	Lys		
	55					60				65							
Met																	
70																	

<210> 7
 <211> 1122
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1122)
 <223>

atg	agc	ggg	gaa	tca	atg	aat	ttc	agc	gat	gtt	ttc	gac	tcc	agt	gaa	48	
Met	Ser	Gly	Glu	Ser	Met	Asn	Phe	Ser	Asp	Val	Phe	Asp	Ser	Ser	Glu		
1			5					10					15				
gat	tat	ttt	gtg	tca	gtc	aat	act	tca	tat	tac	tca	gtt	gat	tct	gag	96	
Asp	Tyr	Phe	Val	Ser	Val	Asn	Thr	Ser	Tyr	Tyr	Ser	Val	Asp	Ser	Glu		
		20					25					30					
atg	tta	ctg	tgc	tcc	ttg	cag	gag	gtc	agg	cag	ttc	tcc	agg	cta	ttt	144	
Met	Leu	Leu	Cys	Ser	Leu	Gln	Glu	Val	Arg	Gln	Phe	Ser	Arg	Leu	Phe		
		35				40					45						
gta	ccg	att	gcc	tac	tcc	ttg	atc	tgt	gtc	ttt	ggc	ctc	ctg	ggg	aat	192	
Val	Pro	Ile	Ala	Tyr	Ser	Leu	Ile	Cys	Val	Phe	Gly	Leu	Leu	Gly	Asn		

50	att ctg gtg gtg atc acc ttt gct ttt tat aag aag gcc agg tct atg	240
65	Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met	
70	aca gac gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt	288
85	Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val	
90	ctt act ctc cca ttc tgg gca gtg agt cat gcc act ggt gcg tgg gtt	336
100	Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val	
105	ttc agc aat gcc acg tgc aag ttg cta aaa ggc atc tat gcc atc aac	384
110	Phe Ser Asn Ala Thr Cys Lys Leu Lys Gly Ile Tyr Ala Ile Asn	
115	ttt aac tgc ggg atg ctg ctc ctg act tgc att agc atg gac cgg tac	432
120	Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr	
125	atc gcc att gta cag gcg act aag tca ttc cgg ctc cga tcc aga aca	480
130	Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr	
135	cta ccg cgc agc aaa atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc	528
140	Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val	
145	atc atc tcc agc tca act ttt gtc ttc aac caa aaa tac aac acc caa	576
150	Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln	
155	ggc agc gat gtc tgt gaa ccc aag tac cag act gtc tcg gag ccc atc	624
160	Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile	
165	agg tgg aag ctg ctg atg ttg ggg ctt gag cta ctc ttt ggt ttc ttt	672
170	Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Phe Gly Phe Phe	
175	atc cct ttg atg ttc atg ata ttt tgt tac acg ttc att gtc aaa acc	720
180	Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr	
185	ttg gtg caa gct cag aat tct aaa agg cac aaa gcc atc cgt gta atc	768
190	Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile	
195	ata gct gtg gtg ctt gtg ttt ctg gct tgt cag att cct cat aac atg	816
200	Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met	
205	gtc ctg ctt gtg acg gct gca aat ttg ggt aaa atg aac cga tcc tgc	864
210	Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys	
215	cag agc gaa aag cta att ggc tat acg aaa act gtc aca gaa gtc ctg	912
220	Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu	
225	gct ttc ctg cac tgc tgc ctg aac cct gtg ctc tac gct ttt att ggg	960
230	Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly	
235	cag aag ttc aga aac tac ttt ctg aag atc ttg aag gac ctg tgg tgt	1008
240	Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys	
245	gtg aga agg aag tac aag tcc tca ggc ttc tcc tgt gcc ggg agg tac	1056
250	Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr	
255	tca gaa aac att tct cgg cag acc agt gag acc gca gat aac gac aat	1104
260	Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr Ala Asp Asn Asp Asn	

355
gcg tcg tcc ttc act atg
Ala Ser Ser Phe Thr Met

360

365

1122

370

<210> 8
<211> 374
<212> PRT
<213> Homo sapiens

<400> 8
Met Ser Gly Glu Ser Met Asn Phe Ser Asp Val Phe Asp Ser Ser Glu
1 5 10 15
Asp Tyr Phe Val Ser Val Asn Thr Ser Tyr Tyr Ser Val Asp Ser Glu
20 25 30
Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
35 40 45
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
50 55 60
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
65 70 75 80
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
85 90 95
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
100 105 110
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
115 120 125
Phe Asn Cys Gly Met Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
130 135 140
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
145 150 155 160
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
165 170 175
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
180 185 190
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
195 200 205
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe
210 215 220
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr
225 230 235 240
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
245 250 255
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met
260 265 270
Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
275 280 285
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
290 295 300
Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
305 310 315 320
Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
325 330 335
Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr
340 345 350
Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr Ala Asp Asn Asp Asn
355 360 365
Ala Ser Ser Phe Thr Met

370

<210> 9
 <211> 1101
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(1101)
 <223>

<400> 9
 atg aat tcc aca gag tcc tac ttt gga acg gat gat tat gac aac aca 48
 Met Asn Ser Thr Glu Ser Tyr Phe Gly Thr Asp Asp Tyr Asp Asn Thr
 1 5 10 15
 gag tat tat tct att cct cca gac cat ggg cca tgc tcc cta gaa gag 96
 Glu Tyr Tyr Ser Ile Pro Pro Asp His Gly Pro Cys Ser Leu Glu Glu
 20 25 30
 gtc aga aac ttc acc aag gta ttt gtg cca att gcc tac tcc tta ata 144
 Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
 35 40 45
 tgt gtc ttt ggc ctc ctg ggc aac att atg gtg gtg atg acc ttt gcc 192
 Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
 50 55 60
 ttc tac aag aaa gcc aga tcc atg act gac gtc tac ctg ttg aac atg 240
 Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
 65 70 75 80
 gcc atc aca gac ata ctc ttt gtc ctc acc cta ccg ttc tgg gca gtt 288
 Ala Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val
 85 90 95
 act cat gcc acc aac act tgg gtt ttc agc gat gca ctg tgt aaa ctg 336
 Thr His Ala Thr Asn Thr Trp Val Phe Ser Asp Ala Leu Cys Lys Leu
 100 105 110
 atg aaa ggc aca tat gcg gtc aac ttt aac tgt ggg atg ctg ctc ctg 384
 Met Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu
 115 120 125
 gcc tgt atc agc atg gac cgg tac att gcc atc gtc cag gca acc aaa 432
 Ala Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys
 130 135 140
 tct ttc cgg gta cgc tcc aga aca ctg acg cac agt aag gtc atc tgt 480
 Ser Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys
 145 150 155 160
 gtg gca gtg tgg ttc atc tcc atc atc atc tca agc cct aca ttt atc 528
 Val Ala Val Trp Phe Ile Ser Ile Ile Ile Ser Ser Pro Thr Phe Ile
 165 170 175
 ttc aac aag aaa tac gag ctg cag gat cgt gat gtc tgt gag cca cgg 576
 Phe Asn Lys Lys Tyr Glu Leu Gln Asp Arg Asp Val Cys Glu Pro Arg
 180 185 190
 tac agg tct gtc tca gag ccc atc acg tgg aag ctg ctg ggt atg gga 624
 Tyr Arg Ser Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly
 195 200 205
 ctg gag ctg ttc ttt ggg ttc ttc acc cct ttg ctg ttt atg gtg ttc 672
 Leu Glu Leu Phe Phe Gly Phe Phe Thr Pro Leu Leu Phe Met Val Phe
 210 215 220
 tgc tat ctg ttc att atc aag acc ttg gtg cag gcc cag aac tcc aag 720
 Cys Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys

225		230		235		240	
agg cac aga gcc atc cga gtc gtg atc gct gtg gtt ctc gtg ttc ctg	768						
Arg His Arg Ala Ile Arg Val Val Ile Ala Val Val Leu Val Phe Leu							
		245		250		255	
gct tgt cag atc cct cac aac atg gtc ctc ctc gtg act gcg gtc aac	816						
Ala Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Val Asn							
		260		265		270	
acg ggc aaa gtg ggc cgg agc tgc agc acc gag aaa gtc ctc gcc tac	864						
Thr Gly Lys Val Gly Arg Ser Cys Ser Thr Glu Lys Val Leu Ala Tyr							
		275		280		285	
acc agg aac gtg gcc gag gtc ctg gct ttc ctg cat tgc tgc ctc aac	912						
Thr Arg Asn Val Ala Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn							
		290		295		300	
ccc gtg ttg tat gcg ttt att gga cag aaa ttc aga aac tac ttc atg	960						
Pro Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Asn Tyr Phe Met							
		305		310		315	
aag atc atg aag gat gtg tgg tgt atg aga agg aag aat aag atg cct	1008						
Lys Ile Met Lys Asp Val Trp Cys Met Arg Arg Lys Asn Lys Met Pro							
		325		330		335	
ggc ttc ctc tgt gcc cgg gtt tac tcg gaa agc tac atc tcc agg cag	1056						
Gly Phe Leu Cys Ala Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln							
		340		345		350	
acc agt gag acc gtc gaa aat gat aat gca tcg tcc ttt acc atg	1101						
Thr Ser Glu Thr Val Glu Asn Asp Asn Ala Ser Ser Phe Thr Met							
		355		360		365	

<210> 10
 <211> 367
 <212> PRT
 <213> Mus musculus

<400> 10
 Met Asn Ser Thr Glu Ser Tyr Phe Gly Thr Asp Asp Tyr Asp Asn Thr
 1 5 10 15
 Glu Tyr Tyr Ser Ile Pro Pro Asp His Gly Pro Cys Ser Leu Glu Glu
 20 25 30
 Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
 35 40 45
 Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
 50 55 60
 Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
 65 70 75 80
 Ala Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val
 85 90 95
 Thr His Ala Thr Asn Thr Trp Val Phe Ser Asp Ala Leu Cys Lys Leu
 100 105 110
 Met Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu
 115 120 125
 Ala Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys
 130 135 140
 Ser Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys
 145 150 155 160
 Val Ala Val Trp Phe Ile Ser Ile Ile Ile Ser Ser Pro Thr Phe Ile
 165 170 175
 Phe Asn Lys Lys Tyr Glu Leu Gln Asp Arg Asp Val Cys Glu Pro Arg
 180 185 190
 Tyr Arg Ser Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly

<400> 13

tgtattgaag acagaacact tgtggtaaga caccaccccc cgggagggcg aagaacaagc	60
cacacactgc tttgaagagt ccagcccca gagaactgc aagggcagac actgttcttg	120
ccacctgcag tttgaagtca tcaactttcaa tccccctgtg actagggcca ggggtcttcac	180
acctgcgaga ggaagcaaaag atctaagcaa tctgaatttt aagagagaaa ctgcagctgt	240
cggtttgtgg gccggaacat tattggactg gagcctggac aagcactaag gcgggggtac	300
ctggccagcc cacttcggag ctcagcgttt ccttgggaaa cg atg aat ttc acc	354
Met Asn Phe Thr	
1	
gag gcc aac tac gga atg gaa gat tat act ggc tca gat tac tct atg	402
Glu Ala Asn Tyr Gly Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met	
5 10 15 20	
ttt cca gag acc gag cca tgc tct ctg caa gag gtc aga gac ttc acc	450
Phe Pro Glu Thr Glu Pro Cys Ser Leu Gln Glu Val Arg Asp Phe Thr	
25 30 35	
aag gtg ttc gtg cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc	498
Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu	
40 45 50	
ctt ggc aat att atg gtg gtg ata acc ttt gcc ttc tac aag aaa gcc	546
Leu Gly Asn Ile Met Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala	
55 60 65	
agg tcc atg act gac gtc tac cta ttg aac atg gcc atc aca gac ata	594
Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile	
70 75 80	
ctc ttt gtc ctc acc cta cca ttc tgg gca gtt act cat gcc act gac	642
Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Thr His Ala Thr Asp	
85 90 95 100	
act tgg atc ttt ggc aac acg atg tgt aaa ctg atg aaa ggc acg tat	690
Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met Lys Gly Thr Tyr	
105 110 115	
gcg gtc aac ttt aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg	738
Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met	
120 125 130	
gac cgg tac att gcc atc gtc cag gcg acc aaa tct ttc cgg gta cgc	786
Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Val Arg	
135 140 145	
tcc aga aca ctg acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc	834
Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe	
150 155 160	
gtt tcc atc atc atc tca agc ccc aca ttc ttc ttc aac aag caa tac	882
Val Ser Ile Ile Ile Ser Ser Pro Thr Phe Phe Phe Asn Lys Gln Tyr	
165 170 175 180	
aag ctg cag ggc cgt gat gtc tgc gag cct cag tac aag ctc gtc tcg	930
Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser	
185 190 195	
gag ccc atc acg tgg aaa ctg ctg ggc atg gga ctc gag ctg ctc ttt	978
Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly Leu Glu Leu Leu Phe	
200 205 210	
ggc ttc ttc atc cct ttg ctg ttt atg gtg ttc tgt tac ctg ttc atc	1026
Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys Tyr Leu Phe Ile	
215 220 225	
atc aag acc ttg gtg cag gcc cag aat tcc aag agg cac aga gcc atc	1074
Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile	
230 235 240	
cga gtc gtg att gct gtg gtt ctc gtg ttc ctg gct tgt cag atc cct	1122
Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro	

245	250	255	260	
cac aac atg gtc ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc				1170
His Asn Met Val Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly				
	265	270	275	
cgc agc tgc agc gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct				1218
Arg Ser Cys Ser Ala Glu Lys Ala Leu Ala Tyr Ala Arg Asn Val Ala				
	280	285	290	
gag gtc ctg gct ttc ctg cac tgc tgt ctc aac ccc gtg ttg tat gcc				1266
Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala				
	295	300	305	
ttc att gga cag aaa ttc aga agc tac ttc atg aag atc atg aag gat				1314
Phe Ile Gly Gln Lys Phe Arg Ser Tyr Phe Met Lys Ile Met Lys Asp				
	310	315	320	
gtg tgg tgt atg agg agg aag agc aag gtg cct acc ttc ttc tgt gcc				1362
Val Trp Cys Met Arg Arg Lys Ser Lys Val Pro Thr Phe Phe Cys Ala				
	325	330	335	340
cgg gtt tac tca gaa agc tac atc tcc agg cag acc agt gag act gta				1410
Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val				
	345	350	355	
gaa aat gac aac gca tcg tcc ttt acc atg taa cacgagagca caaagcagca				1463
Glu Asn Asp Asn Ala Ser Ser Phe Thr Met				
	360	365		
tgccccgaaa gcctttgtga aacttgctat tacatgtga				1502

<210> 14
 <211> 366
 <212> PRT
 <213> Rattus norvegicus

<400> 14

Met Asn Phe Thr Glu Ala Asn Tyr Gly Met Glu Asp Tyr Thr Gly Ser	
1 5 10 15	
Asp Tyr Ser Met Phe Pro Glu Thr Glu Pro Cys Ser Leu Gln Glu Val	
20 25 30	
Arg Asp Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys	
35 40 45	
Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Ile Thr Phe Ala Phe	
50 55 60	
Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala	
65 70 75 80	
Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Thr	
85 90 95	
His Ala Thr Asp Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met	
100 105 110	
Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu Ala	
115 120 125	
Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser	
130 135 140	
Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys Leu	
145 150 155 160	
Thr Val Trp Phe Val Ser Ile Ile Ile Ser Ser Pro Thr Phe Phe Phe	
165 170 175	
Asn Lys Gln Tyr Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr	
180 185 190	
Lys Leu Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly Leu	
195 200 205	
Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys	

210		215		220
Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg				
225		230		235
His Arg Ala Ile Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala				240
		245		250
Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Thr				255
		260		265
Gly Lys Met Gly Arg Ser Cys Ser Ala Glu Lys Ala Leu Ala Tyr Ala				270
		275		280
Arg Asn Val Ala Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro				285
		290		295
Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Ser Tyr Phe Met Lys				300
		305		310
Ile Met Lys Asp Val Trp Cys Met Arg Arg Lys Ser Lys Val Pro Thr				315
		320		325
Phe Phe Cys Ala Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln Thr				330
		335		340
Ser Glu Thr Val Glu Asn Asp Asn Ala Ser Ser Phe Thr Met				345
		350		355
		360		365

<210> 15
 <211> 1309
 <212> DNA
 <213> Rattus norvegicus (liver)

<220>
 <221> CDS
 <222> (150)..(1250)
 <223>

<400> 15	
gcattctcact acccgtctct caatgagcac cgctggttgt gcctgtcaac agaatagtcc	60
tctcacactt aggactggag cctggacaag cactaaggcg ggggtacctg gccagcccac	120
ttcggagctc agcgtttcct tgggaaacg atg aat ttc acc gag gcc aac tac	173
	Met Asn Phe Thr Glu Ala Asn Tyr
	1 5
gga atg gaa gat tat act ggc tca gat tac tct atg ttt cca gag acc	221
Gly Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met Phe Pro Glu Thr	
	10 15 20
gag cca tgc tct ctg caa gag gtc aga gac ttc acc aag gtg ttc gtg	269
Glu Pro Cys Ser Leu Gln Glu Val Arg Asp Phe Thr Lys Val Phe Val	
	25 30 35 40
cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc ctt ggc aat att	317
Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn Ile	
	45 50 55
atg gtg gtg ata acc ttt gcc ttc tac aag aaa gcc agg tcc atg act	365
Met Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met Thr	
	60 65 70
gac gtc tac cta ttg aac atg gcc atc aca gac ata ctc ttt gtc ctc	413
Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile Leu Phe Val Leu	
	75 80 85
acc cta cca ttc tgg gca gtt act cat gcc act gac act tgg atc ttt	461
Thr Leu Pro Phe Trp Ala Val Thr His Ala Thr Asp Thr Trp Ile Phe	
	90 95 100
ggc aac acg atg tgt aaa ctg atg aaa ggc acg tat gcg gtc aac ttt	509
Gly Asn Thr Met Cys Lys Leu Met Lys Gly Thr Tyr Ala Val Asn Phe	
	105 110 115 120

aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg gac cgg tac att	557
Asn Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met Asp Arg Tyr Ile	
125 130 135	
gcc atc gtc cag gcg acc aaa tct ttc cgg gta cgc tcc aga aca ctg	605
Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Val Arg Ser Arg Thr Leu	
140 145 150	
acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc gtt tcc atc atc	653
Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe Val Ser Ile Ile	
155 160 165	
atc tca agc ccc aca ttc ttc ttc aac aag caa tac aag ctg cag ggc	701
Ile Ser Ser Pro Thr Phe Phe Phe Asn Lys Gln Tyr Lys Leu Gln Gly	
170 175 180	
cgt gat gtc tgc gag cct cag tac aag ctc gtc tcg gag ccc atc acg	749
Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser Glu Pro Ile Thr	
185 190 195 200	
tgg aaa ctg ctg ggc atg gga ctc gag ctg ctc ttt ggc ttc ttc atc	797
Trp Lys Leu Leu Gly Met Gly Leu Glu Leu Leu Phe Gly Phe Phe Ile	
205 210 215	
cct ttg ctg ttt atg gtg ttc tgt tac ctg ttc atc atc aag acc ttg	845
Pro Leu Leu Phe Met Val Phe Cys Tyr Leu Phe Ile Ile Lys Thr Leu	
220 225 230	
gtg cag gcc cag aat tcc aag agg cac aga gcc atc cga gtc gtg att	893
Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile Arg Val Val Ile	
235 240 245	
gct gtg gtt ctc gtg ttc ctg gct tgt cag atc cct cac aac atg gtc	941
Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met Val	
250 255 260	
ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc cgc agc tgc agc	989
Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly Arg Ser Cys Ser	
265 270 275 280	
gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct gag gtc ctg gct	1037
Ala Glu Lys Ala Leu Ala Tyr Ala Arg Asn Val Ala Glu Val Leu Ala	
285 290 295	
ttc ctg cac tgc tgt ctc aac ccc gtg ttg tat gcc ttc att gga cag	1085
Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly Gln	
300 305 310	
aaa ttc aga agc tac ttc atg aag atc atg aag gat gtg tgg tgt atg	1133
Lys Phe Arg Ser Tyr Phe Met Lys Ile Met Lys Asp Val Trp Cys Met	
315 320 325	
agg agg aag agc aag gtg cct acc ttc ttc tgt gcc cgg gtt tac tca	1181
Arg Arg Lys Ser Lys Val Pro Thr Phe Phe Cys Ala Arg Val Tyr Ser	
330 335 340	
gaa agc tac atc tcc agg cag acc agt gag act gta gaa aat gac aac	1229
Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val Glu Asn Asp Asn	
345 350 355 360	
gca tcg tcc ttt acc atg taa cacgagagca caaagcagca tgccccgaaa	1280
Ala Ser Ser Phe Thr Met	
365	
gcctttgtga aacttgctat tacatgtga	1309

<210> 16

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Oligonucleotide designed to act as primer for amplifying CCR6

cDNA derived from rat kidney.

<400> 16
tgtattgaag acagaacact tgtgg 25

<210> 17
<211> 28
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying CCR6
cDNA derived from rat kidney or rat liver.

<400> 17
tcacatgtaa tagcaagttt caciaaagg 28

<210> 18
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying CCR6
cDNA derived from rat liver.

<400> 18
gcattctcact acccgtctct c 21

<210> 19
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying fragment
of rat CCR6 gene transcript.

<400> 19
ggacgatgcg ttgtcatttt c 21

<210> 20
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying fragment
of rat CCR6 gene transcript.

<400> 20
ccgcagctgc agcgccgaga aa 22

<210> 21
<211> 20
<212> DNA
<213> Artificial

<220>

<223> Oligonucleotide designed to act as primer for amplifying fragment
of rat CCR6 gene transcript.

<400> 21

gtgcccgggt ttactcagaa

20